

Figure 1A

1	CGGACCCGTGGCGCGCAGCCTGGCTGACCTGATCCTGGACCAAGTGC	60
61	CGCUGGTGCCGCAAGATGCTGGGCCAGCGCAGGGCTGCTCTTCA	120
1	PCTGGAAOGGGCGCGG I L A Q P D R L L F I L D G A D	16
121	CGGAGCTGCCCGCGCGCTGGGGGGCGCGGAGGCGCGGCCCTGACAGAACCGCTTGAGAGCGCG	180
17	E L P A L G G P E A A P C T D P F E A A	36
181	CGAGCGGCGCGCGGGCTGCTAGGCCTGGCTGCTGAGTAAGGGCGCTGCTGCCAACGGCCCTGC	240
37	S G A R E M L G S L L S K A L E P T A L L	56
241	TGCTGGTACCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	300
57	L V T G L R A A A P S R L Q G R C C S P Q	76
361	AATGCGCGAGGTGCGGGCGCTTCCTGGACAAGAACAAAGAAAGTATTCTACAAAGTTGT	360
77	C A E V R G F S D K D K K K Y F Y K F F	96
361	T CGGGATGAGAGGAGGGCGAGCGCGCTCACCGCTTGTGAAGGAGAACAGACCGCTGT	420
97	R D E R R A E R A Y R F V K H N E T L E	116
421	T CGGGCTGTGCTTGGTGGCGCTTCCTGGTGCCTGGATCGTGTGACCGCTGCTGCCAGCG	480
117	A L S E F M P E V C W T V C T N L R Q Q S	136
481	TGGAGCTGGTGGAGACTGTGCGCGACGTCCTAGACCACACGGTCACTGTAACTGCTTT	540
137	E L G P D L S F T S H T T T S M Y L L E	156
541	T CATCACCAAGCGTTCTGAGCTCGCTCCGATAACCGACGGCCCGGGTGCAGGGCGACC	600
157	I T S V L S S A P V A D G P R L Q G D L	176
601	TGGCAATCTGCGCGCGCTGGCGAGGGCGCTGGACGCCAGGGCGACTTTGCCG	660
177	R N L C H L A F E G V L G R R A Q F A E	196
661	AGAAGGAACCTGCAGAACCTGGAGCTTGGTGGCTCCAAAGTGCAGAGCTGTTCTCAGCA	720
197	K E L P Q L E L R G S K V Q T L F L S K	216
781	AAAATGAGTGGCGCGCTGGAGACAGAGGTACCTACCGTTCATGGACCCAGAGCT	780
217	K E L P G V L E T E V T Y Q F T D Q S F	236
781	TCCAGGAGTTCTCGCGCACTGCTACCTGGTGGAGGACGGCGGGGTGCCAGGACCG	840
237	G E F L A A L S Y L L E I G G V P P T A	256
841	CGAATGGCGCGCTGGACAGAGGTACCTGGTGGAGGACGGCGGGGTGCCAGGACCG	900
237	A G S V G T I L P G P A Q F H S H L V I	276

**Figure 1B**

901 277	TCACCACGCGCTTCCCTTTCGGACTGCTGAGCGCGGAGCGGATGCGCGACATCGAGCGC T T R F L F G L L S A E F M R D I E R H	960 296
961 297	ACTTCGGCTGCATGGTTTCAGAGCGTGTGAAGCAGGAGGCCCTGGCGTGGGTGCAGGGAC F G C H V S E R V K Q E A L R W V Q G Q	1020 316
1021 317	AGGGACAGGGCTGCCCCGGAGTGCGACAGGAGGTGACCGAGGGGGCAAAAGGGCTGGAGG G Q G C P G V A P E V T E G A K R G L E D	1080 356
1081 337	ACACCGAAGAGGCCAGAGGAGGGAGGGAGAGGAGGCCAACCTACCCACTGGAGITGC C H E P E E E E M G E E P N Y P L E L L	1140 356
1141 357	TGTACTGCGTGTACGAGACCGCAGGAGCGCTTGCGCCAAAGCCCTGTGCGGGCTGC Y C L Y E T Q E D A F V E Q A L C R F P	1100 376
1201 377	CGGAGCTGGCGCTGCGAGCGTGGCTTCTGCGCATGGACGGCTGTGCTGAGGCGACT E L A L P R V R F C R M D V A V L S Y S	1260 396
1261 397	GCGTCAGGTGCTGCTCTGCTGGAGGGCACTGGCGCTGATCAGCTGCAGATTGGTTGCTG V R C C P A G Q A L R L I S C R L V A A	1320 416
1321 417	CGCACGGAGAAAGAAGAAGAGCTGGGGAAAGGGCTGAGGCCAGGCGCTGGGTGGCGAGCA Q E F K K K S L G V R L Q A I L G C S S	1380 436
1381 437	GTTCTCAAGGCACACACAAATGCGCAGGCTCCCTTCTTCATGCACTCTTTCAGGCGAA S Q G T I K Q L P A S L I H P L F Q A M	1440 456
1441 457	TGACTGACCCACTGIGCCATCTGAGCGAGGCTCACGCTGCCCCTGCAACTGCAANCTCCCTGAGG T D P L H L S S L T L S H C K L P D A	1500 476
1501 477	CGGTCTGCCAGACCTTCTGAGGCCCTGAGGCCCTGAGGGCAGCCCGCACTGACGGAGCTGGCG V C R D I S E A L R A A P A L T E L G L	1560 496
1561 497	TCTTCCACAAACAGGGCTCACTGAGGCGGGACTGCGTATGTTGAGTGAGGGCGTAGCGCTGGC L H N R I S E A G L F M L S E G L A W P	1620 516
1621 517	CGCAGTGCAAGGGTGCAGACGGCTGAGGGTACAGCTGCGCTGACCCCCAGCGAGGGCTGAGT Q C R V Q T V R V Q L P D P Q R G L Q Y	1680 536
1681 537	ACCTCGTGGGTATGCTTCGGCAAGACCCCCGGCGCTGACCCACCTGCGATCTGAGGGCGCTGC L V G H L R Q S P A L T T L P L S G C Q	1740 556
1741 557	AACTTGGCGCGCTATGATGTTGTTGTTGTTGATGCTGCGAGGAGGAGGAGGAGGAGGAGG L I A P M V T T L S A V L V H Q G J G L	1800 576

**Figure 1C**

**Figure 2A**

HLRRS11  
 caspase\_recruitment\_protein  
 cryopyrin  
 Nucleotide\_Binding\_site  
 51  
 (1) MAGGAWGRIACYLEKKEELIEFOLIANKAHRSRSSSGETPAPEEITSC  
 (1) -MASTRCKLARYLEEDVDLIIFPMHEDYPIQKGCIPRPGCTEFADH  
 (1) ---MGFNEQALLECSQDELSEFRYLTTFSAHELOKIPHKEVDKADG  
 100  
 HLRRS11  
 caspase\_recruitment\_protein  
 cryopyrin  
 Nucleotide\_Binding\_site  
 101  
 (1) MEVESTIVAQYGEORANDLAINTWECMGLRSECAQHQEGAGHSPEFPYSP  
 (51) (51) MEVESTIVAQYGEORANDLAINTWECMGLRSECAQHQEGAGHSPEFPYSP  
 (50) VDLATLIMIDENGEEKAWAMAWWIFAAINERRDLYEKAERDEPFWGSNDANW  
 (47) KQEVEITPTHCDSYWVEMASAEQVFEKPHMDLSPRAYDEVFEALKSFHN  
 150  
 HLRRS11  
 caspase\_recruitment\_protein  
 cryopyrin  
 Nucleotide\_Binding\_site  
 151  
 (1) SEPHLGEPSQPTSTAVLMPWIHELPAGCTQGSERRVLEQLEDTSGEEWEH  
 (101) (101) SEPHLGEPSQPTSTAVLMPWIHELPAGCTQGSERRVLEQLEDTSGEEWEH  
 (100) SN-----  
 (97) RK-----  
 200  
 HLRRS11  
 caspase\_recruitment\_protein  
 cryopyrin  
 Nucleotide\_Binding\_site  
 201  
 (1) ISASHLYQALPSSPDHESPSQESPNAPTSTAVLGSWGSPPCDSLAFEQE  
 (151) (151) ISASHLYQALPSSPDHESPSQESPNAPTSTAVLGSWGSPPCDSLAFEQE  
 (102) -----PTVICCGEDS  
 (99) -----PLSLGICR-  
 250  
 HLRRS11  
 caspase\_recruitment\_protein  
 cryopyrin  
 Nucleotide\_Binding\_site  
 251  
 (1) -----  
 (201) APGTQWFLLEETSGIYYTEIFERERESEKGRPPWAAVGTFDGHSSLOP  
 (111) -----TREWMQMLEYLSRISICFMKEDYRKYRKYVRSRFQCLIEENPLGESV  
 (107) PERPPPLEVCEMLERFFFIAQDKEDNRCRYILKTKFREMWSWPGDSHEVQV  
 300  
 HLRRS11  
 caspase\_recruitment\_protein  
 cryopyrin  
 Nucleotide\_Binding\_site  
 301  
 (1) -----  
 (201) HHHFWEPFVRESLCSTWPWNEEDFNFQPFYQILLLQRPWPRSCDPLVFRSW  
 (111) -----SLNKPYTLELRLLFEEHRSQHRECELLAIGETPTCESPV-----  
 (157) HAERYHMLIIPFSNPR-----  
 350  
 HLRRS11  
 caspase\_recruitment\_protein  
 cryopyrin  
 Nucleotide\_Binding\_site  
 351  
 (1) -----  
 (201) FDYVEEENFGHLIETRDLFGFGLDTQEPRIYILOGAAGIGHFLAROVKEA  
 (199) -----SPIKMELLFDPPDEHSEPVHTVVFGAAAGIGHFLARFMDL  
 (172) -----VEPGPFSYTVVLYGPAIGLGYTLAQKILKD  
 400  
 HLRRS11  
 caspase\_recruitment\_protein  
 cryopyrin  
 Nucleotide\_Binding\_site  
 401  
 (1) -----  
 (201) WGRGOLYGERFOHVFYFSCRELAQSKVVSLAELIGKSTATPAPFCILS  
 (241) WASSTYKCREDFDLYFIHREVSLSVTQSSGDMMSCCPDENPCHKLVK  
 (202) WAEDNLIIHK-EKSAVNLSCFELSRLGPQSEEVVFRDWPBLODDFEEHLA  
 450  
 HLRRS11  
 caspase\_recruitment\_protein  
 cryopyrin  
 Nucleotide\_Binding\_site  
 451  
 (1) QPNRLFILLEGAEEDP-AIGGPEAAPCTPFEASGARVLCGELSHALIP  
 (401) RPERLFLPMLGCVDPFWVCEPSSSELCHSQOPADALGSNIGHTILE  
 (241) FPSRILFLMGGFEDQCFDEHGPCTPQFAERSEI-LSSIEIPFELP  
 (202) CAPKILFVIDGFIELDGAPGAIKEDIDGEWEFKFPVVLQSLINFVMLP  
 500  
 HLRRS11  
 caspase\_recruitment\_protein  
 cryopyrin  
 Nucleotide\_Binding\_site  
 501  
 (1) -----  
 (201) QALILVTPAARPGRLGRGCSPOCAEWRCGSDKPKKTFKPFDPFPR  
 (451) EASPLIPARTTAQNLIIPSLEQAPKNEVLGFSSESSRKEFVTFRTDEFCIA  
 (241) EASLIEITPPVVAEKSCHEEDHFRHIEILGFSEAKRPEEKFKEFSEACQ  
 (202) KAAALVTPPRAIRDRJAAPEPIYIRPGECLLEDKRAASLRHFGEDCQ  
 550  
 HLRRS11  
 caspase\_recruitment\_protein  
 cryopyrin  
 Nucleotide\_Binding\_site  
 551  
 (1) -----  
 (201) PRAYPFVRENELFLALCFVPFWCWLNTVPRQOLELGRDLSRFSFTTTSV  
 (451) IPRAPFLVNSKELWALCLFWNSLACTGCMQMKRKEKLTISSTTTITL  
 (241) FAASLQIQLGENEVLTMCHIPLKWCWVCTLPQOMSCKSLACTSKTTAV  
 (202) MRAPFLMRSNAALPQGQAPAVCWVCTTFLQMEKGEDPWEFCITRFGL  
 600  
 HLRRS11  
 caspase\_recruitment\_protein  
 cryopyrin  
 Nucleotide\_Binding\_site  
 601  
 (1) -----  
 (201) YLFITSVLSSAPVADGPFLLGPRRLQLPAPREGVGLGRRAEAEKELEQ  
 (451) GLYLAQALCA,P-----LGPOLRLQLCSLAAEGIWKSTLSEFDOLRKH  
 (241) YLFITSVLSSQPLQPGGSGCNGLCAHNGLQLSLAADGIWNQKLEFESDLRNH  
 (202) FFLFLQSFPEF-----OGAALLEGALRISLLAAQGLWAQTSVLUFREDLRL

Figure 2B

HLRPS11  
caspase\_recruitment\_protein  
cryopyrin  
Nucleotide\_Binding\_Site

(202) EHRGSKVOTLFLSKKEIFGVLETEVTYQFIDQSFQEFIAALSYLEEDGGV  
(591) GLDGAIISTFLKG--ILQEHPIPLSYSFIHLCFQEFAAMSYVLEDEP-  
(491) GLQKADVSASFIRN-LFQKEVDCEKFVSPFHMTFQEFFFAMYLLEEEKE  
(446) GMQESDLRLFEDGQ-ILEQDRVSKGCYSFIHLSFQQFLTALFYTLEKEEE

601 650  
(159) PRTAAGG-----VGTLLRGDAQPHSHIVLTTRFLFGLISAEFRD  
(641) -----GEGFHSNIIIDLEKTLEAYGINGLEGASTTRFLGLISDEGERE  
(546) GRTNVPGSFLKLPFEDVTLLEN:GKFEKGYLIFVVRFLFGLVNCERTSY  
(491) EDDRDGHTWIG---DVCKLLSGVERLRNPDLIQAGYYSGCINERRAKE

651 700  
(193) IERHEGCMVSEVERQEAELRWVOG:GQNCFGVAPEVTEGAKGLEDTEEPHE  
(496) MENIFHCRILSS-CRNLIMQAVPSI-----QLLLOPHS-----  
(190) LEFKLSCSKISQ-CRLEELKMTIEV-----ANAKKLDIQFCQ  
(431) LEATFGCRMSPDIIKQELLRCDIS-----KGGRSTVTBLO

701 750  
(143) EEEGEEEPNNPFLELLYCLYETQEDA:FYRVALCRFPPELAQRVRFQFMDFMVAV  
(165) -----LESLEHCLYETRNK:FLTVMAHFFEMGMG-VEITDMEWV  
(541) -----LEMYCYLYEMQEEEDFVQRAMUYFPKIEIN--LITFRMDHMV  
(771) -----ELIGCLYEQEEELVKEVMAQFHEISLH--DNAVDEVV

751 800  
(100) LSQCPVCPFACQDPHLLISDFRLVAACPFYKSLGKRLQASLGGSQS-----  
(114) CTECICIPSRHVKHICLLEGRQHESTWFSMSWVIFPWVPVTDAIWQILES-  
(644) SSFCIENCHFVNEESLGLFHNMPKEEEEEEGRHLDMVOCVLESSHAA  
(611) SSFCVRRHCRMLQHMSIQLVIKENLPENNTASESDAEVERSODDQHMLPWT

801 850  
(119) -----  
(111) -----  
(114) QSHGLVNNSH-----  
(666) DLSGSIFNSNPKDEMGLAINDSFLSASIVFILEQIASDITCHLQFVVFKKNIS

851 900  
(126) -----GTTKQFASLLHPLFQAMTDEPQCHLSSLET  
(611) -----VTKVTRNLPELDLS.NSLSHSAVKSCLKTLPRPQG:LETLR  
(716) SSPDORGIFSVLTSQSITELDLSINSLGDPGMRVLCETLQHPFCNIRKLW  
(711) PADAHENILCALEGHFTVTVTYLTLQGNWIDDMFFALCEVERHPTCNLRTEQ

901 950  
(118) LSHQKLPDAVCPDLSEALPAAAPALTELQILHNFILSEAGLRMLSEGLAWPQ  
(644) LAGCGGLTAEDCKDIAFGRLRANQITLTEELDSLHVNLMDAGAKHILQQLRQPS  
(116) LQFCGLSHEC-----SISLVESSNOKEVELLSENALGEFGIRLQVGKHLW  
(761) LVSCSATTOQWAIDLSLALEVNQSLTCVNLSDNELLDGAKLLETTLQRHPF

951 1000  
(118) CRVQTVHVQQLPDPQ-FGIQYLVGMRCSPALTILDISGQCPAPMVTYLC  
(644) CQHQRLILVSCGTTSIECQDLASVLSAAPSILKELDLQINNEDWGVVLRLC  
(114) CMKKLWLWVSCGTTTSACCQDLASVLSTHSLTFLYVGENALGDGCVAILC  
(711) CQLQLTLENCHLTETANCKELAAAVLIVSPFTHLCLAKNPICNTGVKFLC

1001 1050  
(167) AVEHQGCGEQLTSEASVELSEQ:IQELQCVKRAFFDEVTHIADGHPQ  
(444) EGGLERPACKLIFLGHIDQTTLSDENRQELPALEQEEPKQLLIFSPRPSVMT  
(751) EFAKNPQCNLQKLGIVNSGLTSVWCSAASSVLISTQNLTLYZRGNTLG  
(622) EGLRYPECKLQTDIWNCDITSLACCLTKLLOEKSSLCCDLCGNHIG

1051 1100  
(161) PPKELISTF-----  
(994) PIEGLDTGEMENSTISSLKRQRLGJERAASHWAQANLKLEDDWSKIFPIAEI  
(925) KCIKLLCEGLLHPECKLQ'LEELINCNLTSHCWDLSTLLTSQSIRKLSI  
(912) RGMKFLCEALRFLCQNLRLQWLWGCSTPPFSCEDLCSALSN-QSLVTLDL

1101 1150  
(617) PPKELISTF-----  
(994) PIEGLDTGEMENSTISSLKRQRLGJERAASHWAQANLKLEDDWSKIFPIAEI  
(925) KCIKLLCEGLLHPECKLQ'LEELINCNLTSHCWDLSTLLTSQSIRKLSI  
(912) RGMKFLCEALRFLCQNLRLQWLWGCSTPPFSCEDLCSALSN-QSLVTLDL

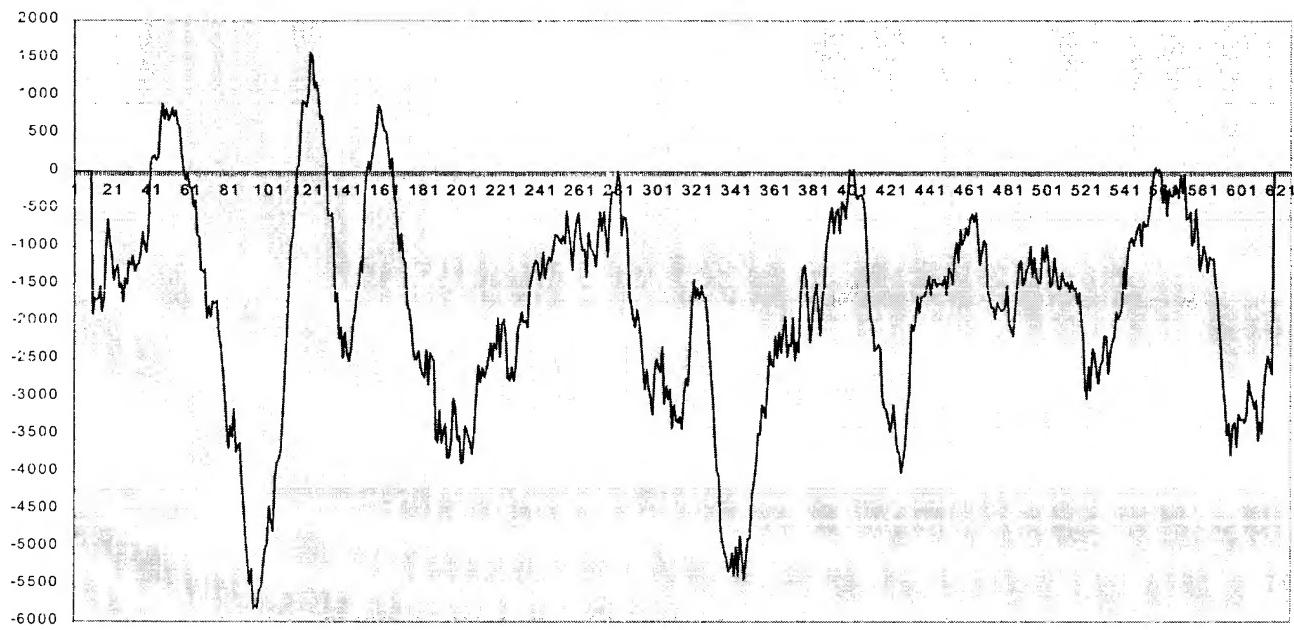
1151 1200  
(606) -----  
(1044) AEESSPVVVPVELLCVPSPASQCDLHTKPLGTDDEFWGPTGPATEBVVDK  
(975) GMN---DLGDIGVMMFCETLKQCSCLQNLGLISEMYFNYPKSALETLOE  
(961) GMN---PLGSSGVMLFEITCOSGTEFTEPLFIDDENDLNKLEEEIEE

**Figure 2C**

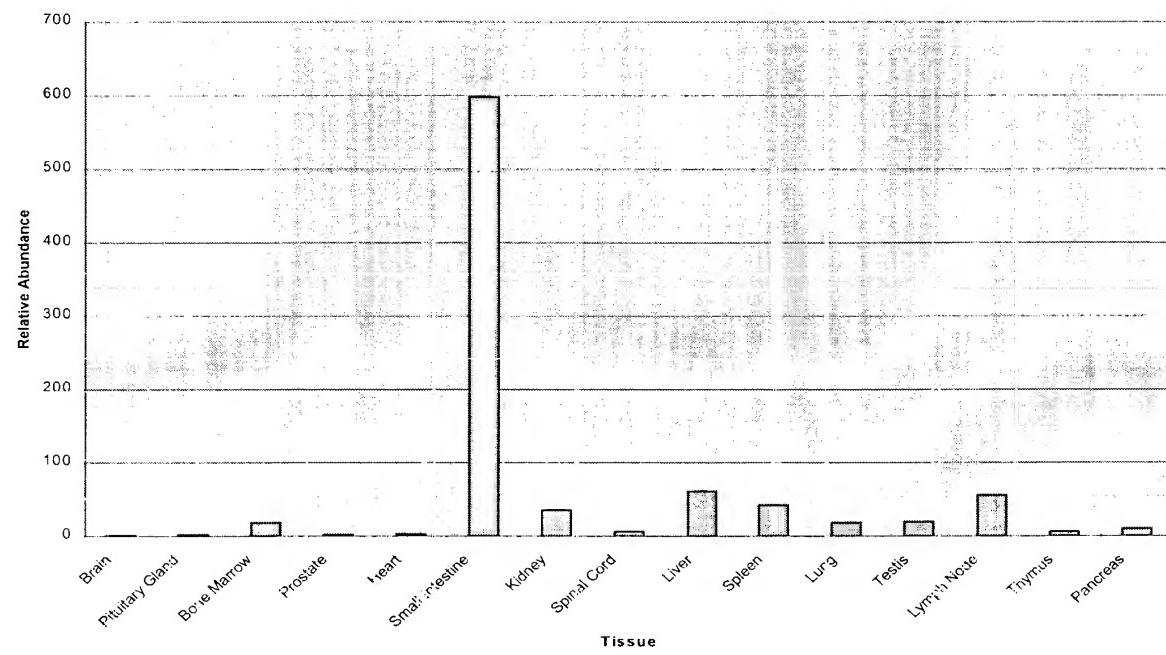
HLRPSI1 caspase_recruitment_protein cryopyrin Nucleotide_Binding_site	1201 (626) ----- (1094) <b>E</b> NLYR <b>T</b> H <b>P</b> VAGSYRWPNNTGLC <b>S</b> VVREAVTVEIEFCVWDQFLGEINPQH (1012) <b>E</b> P <b>E</b> <b>T</b> <b>T</b> V <b>F</b> E <b>P</b> SW----- (1008) <b>K</b> N <b>P</b> <b>O</b> <b>L</b> I <b>I</b> D <b>T</b> E <b>K</b> HH <b>P</b> WA <b>E</b> RPSSHD <b>M</b> I-----	1250
HLRRSI1 caspase_recruitment_protein cryopyrin Nucleotide_Binding_site	1251 (626) ----- (1144) SWMVAGPLLD <b>T</b> AEPGAVEAVHLPHFVALQGGHVDTSLFQVAHFKEEGML (1035) ----- (1034) -----	1300
HLRRSI1 caspase_recruitment_protein cryopyrin Nucleotide_Binding_site	1301 (626) ----- (1194) LEKPARVELHHIVLENPSFSPLGVLLKM1HNALRF1PVTSVVLLYHRLHP (1035) ----- (1034) -----	1350
HLRRSI1 caspase_recruitment_protein cryopyrin Nucleotide_Binding_site	1351 (626) ----- (1144) FEFVTFHLYLIPSDGSIRKELELCYRSPGEDQLFSEFYVGHLGSG1RLQVK (1035) ----- (1034) -----	1400
HLRRSI1 caspase_recruitment_protein cryopyrin Nucleotide_Binding_site	1401 (626) ----- (1194) DHKDETLYWEALVFKGDLMPATTLIPFACIAVPSFLAPQLLHFVDQYRE (1035) ----- (1034) -----	1450
HLRRSI1 caspase_recruitment_protein cryopyrin Nucleotide_Binding_site	1451 (626) ----- (1144) Q1IARVTSNEVVLDPFHGQVLSQPKYEPVIAENTRFSQMRFLFGSLNQWV (1035) ----- (1034) -----	1500
HLRRSI1 caspase_recruitment_protein cryopyrin Nucleotide_Binding_site	1501 (626) ----- (1194) RCKKDGLYQALKETHPHLIMELWEKGSKGKLLPLSS (1035) ----- (1034) -----	1536

D0066 NP

Figure 3



**Figure 4**



D0066 NP

**Figure 5.**

<b>Protein</b>	<b>Genbank ID</b>	<b>Identities</b>	<b>Similarities</b>
human caspase recruitment protein 7	gi 10198209	36.3%	44.0%
human nucleotide binding site protein	gi 10198207	35.0%	42.2%
human cryopyrin protein	gi 17027237	35.7%	46.0%